

1 GAATATGATG ACCCTAATGC AACAAATATCT AACATACTAT CCGAGCTTCG  
51 GTCATTTGGA AGAACTGCAG ATTTTCCTCC TTCAAATAA AAGTCAGGTT  
101 ATGGAGAACA TGTATGCTAT GTTCTTGATT GCTTCGCTGA AGAAGCATTG  
151 AAATATATTG GTTTCACCTG GAAAAGGCCA ATATACCCAG TAGAAGAATT  
201 AGAAGAAGAA AGCGTTGCAG AAGATGATGC AGAATTAACA TTAAATAAAG  
251 TGGATGAAGA ATTTGTGGAA GAAGAGACAG ATAATGAAGA AAACCTTTATT  
301 GATCTCAACG TTTTAAAGGC CCAGACATAT CACTTGGATA TGAACGAGAC  
351 TGCCAAACAA GAAGATATTT TGGAATCCAC AACAGATGCT GCAGAAATGGA  
401 GCCTAGAAGT GGAACGTGTA CTACCGCAAC TGAAAGTCAC GATTAGGACT  
451 GACAATAAGG ATTGGAGAAT CCATGTTGAC CAAATGCACC AGCACAGAAG  
501 TGGAATTGAA TCTGCTCTAA AGGAGACCAA GGGATTTTGT GACAAACTCC  
551 ATAATGAAAT TACTAGGACT TTGGAAAAGA TCAGCAGCCG AGAAAAGTAC  
601 ATCAACAATC AGCCGGGAGC CCATGGAGCA CTGTCCTCAG AGATGCGCAG  
651 GTTAGGCTCA CTGTCTAGGC CAGGCCACC TTAGTCACTG TGGACTGGCA  
701 ATGGAAGCTC TTCCTGGACA CACCTGCCCT AGCCCTCACC CTGGGGTGGG  
751 AGAGAAATGA GCTTGGCTTG CAACTCAGAC CATTCCACGG AGGCATCCTC  
801 CCCTTCCCTG GGCTGGTGAA TAAAAGTTTC CTGAGGTCAA GGAATTCCTT  
851 TTCCCTGCCA AAATGGTGTC CAGAACTTTG AGGCCAGAGG TGATCCAGTG

FIGURE 1A

901    ATTTGGGAGC TGCAGGTCAC ACAGGCTGCT CAGAGGGCTG CTGAACAGGA  
951    TGTCCCTCGGA CGACAGGCAC CTGGGCTCCA GCTGCGGCTC CTTTCATCAAG  
1001   ACTGAGCCGT CCAGCCCGTC CTCGGGCATA GATGCCCTCA GCCACCACAG  
1051   CCCCAGTGGC TCGTCCGACG CCAGCGGCGG CTTTGGCCTG GCCCTGGGCA  
1101   CCCACGCCAA CGGTCTGGAC TCGCCACCCA TGTTTGCAGG CGCCGGGCTG  
1151   GGAGGCACCC CATGCCGCAA GAGCTACGAG GACTGTGCCA GCGGCATCAT  
1201   GGAGGACTCG GCCATCAAGT GCGAGTACAT GCTCAACGCC ATCCCCAAGC  
1251   GCCTGTGCCT CGTGTGCGGG GACATTGCCT CTGGCTACCA CTACGGCGTG  
1301   GCCTCCTGCG AGGCTTGCAA GGCCTTCTTC AAGAGGACTA TCCAAGGGAA  
1351   CATTGAGTAC AGCTGCCCGG CCACCAACGA GTGCGAGATC ACCAAACGGA  
1401   GGCGCAAGTC CTGCCAGGCC TGCCGCTTCA TGAAATGCCT CAAAGTGGGG  
1451   ATGCTGAAGG AAGGTGTGCG CCTTGATCGA GTGCGTGGAG GCCGTCAGAA  
1501   ATACAAGCGA CGGCTGGACT CAGAGAGCAG CCCATACCTG AGCTTACAAA  
1551   TTTCTCCACC TGCTAAAAAG CCATTGACCA AGATTGTCTC ATACCTACTG  
1601   GTGGCTGAGC CGGACAAGCT CTATGCCATG CCTCCCCCTG GTATGCCTGA  
1651   GGGGGACATC AAGGCCCTGA CCACTCTCTG TGACCTGGCA GACCGAGAGC  
1701   TTGTGGTCAT CATTGGCTGG GCCAAGCACA TCCCAGGCTT CTCAAGCCTC  
1751   TCCCTGGGGG ACCAGATGAG CCTGCTGCAG AGTGCCTGGA TGGAAATCCT

FIGURE 1B

1801 CATCCTGGGC ATCGTGTACC GCTCGCTGCC CTACGACGAC AAGCTGGTGT  
1851 ACGCTGAGGA CTACATCATG GATGAGGAGC ACTCCCGCCT CGCGGGGCTG  
1901 CTGGAGCTCT ACCGGGCCAT CCTGCAGCTG GTACGCAGGT ACAAGAAGCT  
1951 CAAGGTGGAG AAGGAGGAGT TTGTGACGCT CAAGGCCCTG GCCCTCGCCA  
2001 ACTCCGATTC CATGTACATC GAGGATCTAG AGGCTGTCCA GAAGCTGCAG  
2051 GACCTGCTGC ACGAGGCACT GCAGGACTAC GAGCTGAGCC AGCGCCATGA  
2101 GGAGCCCTGG AGGACGGGCA AGCTGCTGCT GACACTGCCG CTGCTGCGGC  
2151 AGACGGCCGC CAAGGCCGTG CAGCACTTCT ATAGCGTCAA ACTGCAGGGC  
2201 AAAGTGCCCA TGCACAACT CTCCTGGAG ATGCTGGAGG CCAAGGCCTG  
2251 GGCCAGGGCT GACTCCCTTC AGGAGTGGAG GCCACTGGAG CAAGTGCCCT  
2301 CTCCCCTCCA CCGAGCCACC AAGAGGCAGC ATGTGCATTT CCTAACTCCC  
2351 TTGCCCCCTC CCCCATCTGT GGCCTGGGTG GGCAGTCTC AGGCTGGATA  
2401 CCACCTGGAG GTTTTCCTTC CGCAGAGGGC AGGTTGGCCA AGAGCAGCTT  
2451 AGAGGATCTC CCAAGGATGA AAGAATGTCA AGCCATGATG GAAAATGCCC  
2501 CTTCCAATCA GCTGCCTTCA CAAGCAGGGA TCAGAGCAAC TCCCCGGGGA  
2551 TCCCCAATCC ACGCCCTTCT AGTCCAACCC CCCTCAATGA GAGAGGCAGG  
2601 CAGATCTCAC CCAGCACTAG GACACCAGGA GGCCAGGGAA AGCATCTCTG  
2651 GCTCACCATG TAACATCTGG CTTGGAGCAA GTGGGTGTTC TGCACACCAG  
2701 GCAGCTGCAC CTCACTGGAT CTAGTGTTGC TGCGAGTGAC CTCACTTCAG  
2751 AGCCCCTCTA GCAGAGTGGG GCGGAAGTCC TGATGGTTGG TGTCCATGAG  
2801 GTGGAAG (SEQ ID NO:1)

FIGURE 1C

1 GAATATGATGACCCTAATGCAACAATATCTAACATACTATCCGAGCTTCGGTCATTTGGA 60  
 -----+-----+-----+-----+-----+-----+  
 CTTATACTACTGGGATTACGTTGTTATAGATTGTATGATAGGCTCGAAGCCAGTAAACCT  
 61 AGAACTGCAGATTTTCCTCCTTCAAAATTAAAGTCAGGTTATGGAGAACATGTATGCTAT 120  
 -----+-----+-----+-----+-----+-----+  
 TCTTGACGTCTAAAAGGAGGAAGTTTAAATTCAGTCCAATACCTCTTGTACATACGATA  
 121 GTTCTTGATTGCTTCGCTGAAGAAGCATTGAAATATATTGGTTTACCTGGAAAAGGCCA 180  
 -----+-----+-----+-----+-----+-----+  
 CAAGAACTAACGAAGCGACTTCTTCGTAACCTTTATATAACCAAAGTGGACCTTTCCGGT  
 181 ATATACCCAGTAGAAGAATTAGAAGAAGAAAGCGTTGCAGAAGATGATGCAGAATTAACA 240  
 -----+-----+-----+-----+-----+-----+  
 TATATGGGTCATCTTCTTAATCTTCTTCTTCGCAACGTCTTCTACTACGTCTTAATTGT  
 241 TTAAATAAAGTGGATGAAGAATTTGTGGAAGAAGAGACAGATAATGAAGAAAACCTTTATT 300  
 -----+-----+-----+-----+-----+-----+  
 AATTTATTTACCTACTTCTTAAACACCTTCTTCTGTCTATTACTTCTTTTGAAATAA  
 301 GATCTCAACGTTTTAAAGGCCCGACATATCACTTGGATATGAACGAGACTGCCAAACAA 360  
 -----+-----+-----+-----+-----+-----+  
 CTAGAGTTGCAAAATTTCCGGGTCTGTATAGTGAACCTATACTTGCTCTGACGGTTTGT  
 361 GAAGATATTTTGAATCCACAACAGATGCTGCAGAATGGAGCCTAGAAGTGGAAACGTGTA 420  
 -----+-----+-----+-----+-----+-----+  
 CTTCTATAAAACCTTAGGTGTTGTCTACGACGTCTTACCTCGGATCTTCACCTTGCACAT  
 421 CTACCGCAACTGAAAGTCACGATTAGGACTGACAATAAGGATTGGAGAATCCATGTTGAC 480  
 -----+-----+-----+-----+-----+-----+  
 GATGGCGTTGACTTTCAGTGCTAATCCTGACTGTTATTCCTAACCTCTTAGGTACAACG  
 481 CAAATGCACCAGCACAGAAGTGAATTGAATCTGCTCTAAAGGAGACCAAGGGATTTTGT 540  
 -----+-----+-----+-----+-----+-----+  
 GTTTACGTGGTCTGTCTTCACCTTAACTTAGACGAGATTTCCTCTGGTTCCCTAAAAAC

FIGURE 2A

541 GACAAACTCCATAATGAAATTACTAGGACTTTGGAAAAGATCAGCAGCCGAGAAAAGTAC 600  
 -----+-----+-----+-----+-----+-----+  
 CTGTTTGAGGTATTACTTTAATGATCCTGAAACCTTTTCTAGTCGTCGGCTCTTTTCATG  
  
 601 ATCAACAATCAGCCGGGAGCCCATGGAGCACTGTCTCAGAGATGCGCAGGTTAGGCTCA 660  
 -----+-----+-----+-----+-----+-----+  
 TAGTTGTTAGTCGGCCCTCGGGTACCTCGTGACAGGAGTCTCTACGCGTCCAATCCGAGT  
  
 661 CTGTCTAGGCCAGGCCACCTTAGTCACTGTGGACTGGCAATGGAAGCTCTTCCTGGACA 720  
 -----+-----+-----+-----+-----+-----+  
 GACAGATCCGGTCCGGGTGGAATCAGTGACACCTGACCGTTACCTTCGAGAAGGACCTGT  
  
 721 CACCTGCCCTAGCCCTCACCTGGGGTGGAAGAGAAATGAGCTTGGCTTGCAACTCAGAC 780  
 -----+-----+-----+-----+-----+-----+  
 GTGGACGGGATCGGGAGTGGGACCCACCTTCTCTTTACTCGAACCGAACGTTGAGTCTG  
  
 781 CATTCACGGAGGCATCCTCCCCTTCCCTGGGCTGGTGAATAAAAGTTTCTCTGAGGTCAA 840  
 -----+-----+-----+-----+-----+-----+  
 GTAAGGTGCCTCCGTAGGAGGGGAAGGGACCCGACCACTTATTTTCAAAGGACTCCAGTT  
  
 841 GGACTTCCTTTTCCCTGCCAAAATGGTGTCCAGAACTTTGAGGCCAGAGGTGATCCAGTG 900  
 -----+-----+-----+-----+-----+-----+  
 CCTGAAGGAAAAGGGACGGTTTTACCACAGGTCTTGAAACTCCGGTCTCCACTAGGTCAC  
  
 901 ATTTGGGAGCTGCAGGTACACAGGCTGCTCAGAGGGCTGCTGAACAGGATGTCCTCGGA 960  
 -----+-----+-----+-----+-----+-----+  
 TAAACCCTCGACGTCCAGTGTGTCCGACGAGTCTCCCGACGACTTGTCCTACAGGAGCCT  
 M S S D  
  
 961 CGACAGGCACCTGGGCTCCAGCTGCGGCTCCTTCATCAAGACTGAGCCGTCCAGCCCGTC 1020  
 -----+-----+-----+-----+-----+-----+  
 GCTGTCCGTGGACCCGAGGTCGACGCCGAGGAAGTAGTTCTGACTCGGCAGGTCGGGCAG  
 D R H L G S S C G S F I K T E P S S P S

FIGURE 2B

1021 CTCGGGCATAGATGCCCTCAGCCACCACAGCCCCAGTGGCTCGTCCGACGCCAGCGGCGG 1080  
 -----+-----+-----+-----+-----+-----+  
 GAGCCCGTATCTACGGGAGTCGGTGGTGTCTCGGGGTACCGAGCAGGCTGCGGTGCGCCGCC  
 S G I D A L S H H S P S G S S D A S G G  
  
 1081 CTTTGGCCTGGCCCTGGGCACCCACGCCAACGGTCTGGACTCGCCACCCATGTTTGCAGG 1140  
 -----+-----+-----+-----+-----+-----+  
 GAAACCGGACCGGGACCCGTGGGTGCGGTTGCCAGACCTGAGCGGTGGGTACAAACGTCC  
 F G L A L G T H A N G L D S P P M F A G  
  
 1141 CGCCGGGCTGGGAGGCACCCCATGCCGCAAGAGCTACGAGGACTGTGCCAGCGGCATCAT 1200  
 -----+-----+-----+-----+-----+-----+  
 GCGGCCCCGACCCTCCGTGGGGTACGGCGTTCTCGATGCTCCTGACACGGTCGCCGTAGTA  
 A G L G G T P C R K S Y E D C A S G I M  
  
 1201 GGAGGACTCGGCCATCAAGTGCGAGTACATGCTCAACGCCATCCCCAAGCGCCTGTGCCT 1260  
 -----+-----+-----+-----+-----+-----+  
 CCTCCTGAGCCGGTAGTTCACGCTCATGTACGAGTTGCGGTAGGGGTTTCGCGGACACGGA  
 E D S A I K C E Y M L N A I P K R L C L  
  
 1261 CGTGTGCGGGGACATTGCCTCTGGCTACCACTACGGCGTGGCCTCCTGCGAGGCTTGCAA 1320  
 -----+-----+-----+-----+-----+-----+  
 GCACACGCCCCCTGTAACGGAGACCGATGGTGTATGCCGCACCGGAGGACGCTCCGAACGTT  
V C G D I A S G Y H Y G V A S C E A C K  
  
 1321 GGCCTTCTTCAAGAGGACTATCCAAGGGAACATTGAGTACAGCTGCCCCGGCCACCAACGA 1380  
 -----+-----+-----+-----+-----+-----+  
 CCGGAAGAAGTTCTCCTGATAGGTTCCCTTGTAATCATGTGACGGGCGCGGTGGTTGCT  
A F F K R T I Q G N I E Y S C P A T N E  
  
 1381 GTGCGAGATCACCAACGGAGGCGCAAGTCCTGCCAGGCCTGCCGCTTCATGAAATGCCT 1440  
 -----+-----+-----+-----+-----+-----+  
 CACGCTCTAGTGGTTTGCCTCCGCGTTTCAGGACGGTCCGGACGGCGAAGTACTTTACGGA  
C E I T K R R R K S C Q A C R F M K C L

FIGURE 2C

1441 CAAAGTGGGGATGCTGAAGGAAGGTGTGCGCCTTGATCGAGTGCGTGGAGGCCGTCAGAA 1500  
 -----+-----+-----+-----+-----+-----+  
 GTTTCACCCCTACGACTTCCTTCCACACGCGGAAGTAGCTCACGCACCTCCGGCAGTCTT  
K V G M L K E G V R L D R V R G G R Q K  
 1501 ATACAAGCGACGGCTGGACTCAGAGAGCAGCCCATACCTGAGCTTACAAATTTCTCCACC 1560  
 -----+-----+-----+-----+-----+-----+  
 TATGTTTCGCTGCCGACCTGAGTCTCTCGTCGGGTATGGACTCGAATGTTTAAAGAGGTGG  
 Y K R R L D S E S S P Y L S L Q I S P P  
 1561 TGCTAAAAAGCCATTGACCAAGATTGTCTCATACCTACTGGTGGCTGAGCCGGACAAGCT 1620  
 -----+-----+-----+-----+-----+-----+  
 ACGATTTTTTCGGTAACTGGTTCTAACAGAGTATGGATGACCACCGACTCGGCCTGTTCTGA  
 A K K P L T K I V S Y L L V A E P D K L  
 1621 CTATGCCATGCCTCCCCCTGGTATGCCTGAGGGGGACATCAAGGCCCTGACCACTCTCTG 1680  
 -----+-----+-----+-----+-----+-----+  
 GATACGGTACGGAGGGGGACCATACGGACTCCCCCTGTAGTTCCGGGACTGGTGAGAGAC  
 Y A M P P P G M P E G D I K A L T T L C  
 1681 TGACCTGGCAGACCGAGAGCTTGTGGTCATCATTGGCTGGGCCAAGCACATCCCAGGCTT 1740  
 -----+-----+-----+-----+-----+-----+  
 ACTGGACCGTCTGGCTCTCGAACACCAAGTAGTAACCGACCCGGTTCGTGTAGGGTCCGAA  
 D L A D R E L V V I I G W A K H I P G F  
 1741 CTCAAGCCTCTCCCTGGGGGACCAGATGAGCCTGCTGCAGAGTGCCCTGGATGGAAATCCT 1800  
 -----+-----+-----+-----+-----+-----+  
 GAGTTCGGAGAGGGACCCCCTGGTCTACTCGGACGACGTCTCACGGACCTACCTTTAGGA  
 S S L S L G D Q M S L L Q S A W M E I L  
 1801 CATCCTGGGCATCGTGTACCGCTCGCTGCCCTACGACGACAAGCTGGTGTACGCTGAGGA 1860  
 -----+-----+-----+-----+-----+-----+  
 GTAGGACCCGTAGCACATGGCGAGCGACGGGATGCTGCTGTTTCGACCACATGCGACTCCT  
 I L G I V Y R S L P Y D D K L V Y A E D

FIGURE 2D

1861 CTACATCATGGATGAGGAGCACTCCCGCCTCGCGGGGCTGCTGGAGCTCTACCGGGCCAT 1920  
-----+-----+-----+-----+-----+-----+  
GATGTAGTACCTACTCCTCGTGAGGGCGGAGCGCCCCGACGACCTCGAGATGGCCCGGTA  
Y I M D E E H S R L A G L L E L Y R A I

1921 CCTGCAGCTGGTACGCAGGTACAAGAAGCTCAAGGTGGAGAAGGAGGAGTTTGTGACGCT 1980  
-----+-----+-----+-----+-----+-----+  
GGACGTCGACCATGCGTCCATGTTCTTCGAGTTCCACCTCTTCCTCCTCAAACACTGCGA  
L Q L V R R Y K K L K V E K E E F V T L

1981 CAAGGCCCTGGCCCTCGCCAACTCCGATTCCATGTACATCGAGGATCTAGAGGCTGTCCA 2040  
-----+-----+-----+-----+-----+-----+  
GTTCCGGGACCGGGAGCGGTTGAGGCTAAGGTACATGTAGCTCCTAGATCTCCGACAGGT  
K A L A L A N S D S M Y I E D L E A V Q

2041 GAAGCTGCAGGACCTGCTGCACGAGGCACTGCAGGACTACGAGCTGAGCCAGCGCCATGA 2100  
-----+-----+-----+-----+-----+-----+  
CTTCGACGTCCTGGACGACGTGCTCCGTGACGTCCTGATGCTCGACTCGGTTCGCGGTACT  
K L Q D L L H E A L Q D Y E L S Q R H E

2101 GGAGCCCTGGAGGACGGGCAAGCTGCTGCTGACACTGCCGCTGCTGCGGCAGACGGCCGC 2160  
-----+-----+-----+-----+-----+-----+  
CCTCGGGACCTCCTGCCCCGTTGACGACGACTGTGACGGCGACGACGCCGTCTGCCGGCG  
E P W R T G K L L L T L P L L R Q T A A

2161 CAAGGCCGTGCAGCACTTCTATAGCGTCAAACCTGCAGGGCAAAGTGCCCATGCACAAACT 2220  
-----+-----+-----+-----+-----+-----+  
GTTCCGGCACGTCGTGAAGATATCGCAGTTTGACGTCCCCTTCACGGGTACGTGTTTGA  
K A V Q H F Y S V K L Q G K V P M H K L

2221 CTTCTGAGATGCTGGAGGCCAAGGCCTGGGCCAGGGCTGACTCCCTTCAGGAGTGGAG 2280  
-----+-----+-----+-----+-----+-----+  
GAAGGACCTCTACGACCTCCGGTTCGGGACCCGGTCCCGACTGAGGGAAGTCCTCACCTC  
F L E M L E A K A W A R A D S L Q E W R

FIGURE 2E



9/23

1999Y

2281 GCCACTGGAGCAAGTGCCCTCTCCCTCCACCGAGCCACCAAGAGGCAGCATGTGCATTT  
 -----+-----+-----+-----+-----+-----+ 2340  
 CGGTGACCTCGTTCACGGGAGAGGGGAGGTGGCTCGGTGGTTCTCCGTCGTACACGTAAA  
 P L E Q V P S P L H R A T K R Q H V H F  
  
 2341 CCTAACTCCCTTGCCCCCTCCCCCATCTGTGGCTGGGTGGGCACTGCTCAGGCTGGATA  
 -----+-----+-----+-----+-----+ 2400  
 GGATTGAGGGAACGGGGGAGGGGAGGTAGACACCGGACCCACCCGTGACGAGTCCGACCTAT  
 L T P L P P P P S V A W V G T A Q A G Y  
  
 2401 CCACCTGGAGGTTTTCTTCCGCAGAGGGCAGGTTGGCCAAGAGCAGCTTAGAGGATCTC  
 -----+-----+-----+-----+-----+ 2460  
 GGTGGACCTCCAAAAGGAAGGCGTCTCCCGTCCAACCGGTTCTCGTCGAATCTCCTAGAG  
 H L E V F L P Q R A G W P R A A \* (SEQ ID NO:2)  
  
 CCAAGGATGAAAGAATGTCAAGCCATGATGAAAATGCCCTTCCAATCAGCTGCCTTCA  
 2461 -----+-----+-----+-----+-----+ 2520  
 GGTTCCTACTTTCTTACAGTTCGGTACTACCTTTTACGGGGAAGGTTAGTCGACGGAAGT  
  
 CAAGCAGGGATCAGAGCAACTCCCCGGGGATCCCCAATCCACGCCCTTCTAGTCCAACCC  
 2521 -----+-----+-----+-----+-----+ 2580  
 GTTCGTCCCTAGTCTCGTTGAGGGGCCCTAGGGGTTAGGTGCGGGAAGATCAGGTTGGG  
  
 CCCTCAATGAGAGAGGCAGGCAGATCTCAGGAGCACTAGGACACCAGGAGGCCAGGGAA  
 2581 -----+-----+-----+-----+-----+ 2640  
 GGGAGTTACTCTCTCCGTCCGTCTAGAGTGGGTGCTGATCCTGTGGTCCTCCGGTCCCTT  
  
 AGCATCTCTGGCTCACCATGTAACATCTGGCTTGGAGCAAGTGGGTGTTCTGCACACCAG  
 2641 -----+-----+-----+-----+-----+ 2700  
 TCGTAGAGACCGAGTGGTACATTGTAGACCGAACCTCGTTCACCCACAAGACGTGTGGTC  
  
 GCAGCTGCACCTCACTGGATCTAGTGTGCTGCGAGTGACCTCACTTCAGAGCCCCTCTA  
 2701 -----+-----+-----+-----+-----+ 2760  
 CGTCGACGTGGAGTGACCTAGATCACAACGACGCTCACTGGAGTGAAGTCTCGGGGAGAT  
  
 GCAGAGTGGGGCGGAAGTCCTGATGGTTGGTGTCCATGAGGTGGAAG (SEQ ID NO:1)  
 2761 -----+-----+-----+-----+-----+ 2807  
 CGTCTACCCCGCCTTCAGGACTACCAACCACAGGTACTCCACCTTC (SEQ ID NO:29)

FIGURE 2F

10/23

19999 Y

105444.01302  
MSSDDRHLGS SCGSFIKTEP SSPSSGIDAL SHHSPSGSSD ASGGFGLALG  
THANGLDSPP MFAGAGLGGT PCRKSYEDCA SGIMEDSAIK CEYMLNAIPK  
RLCLVCGDIA SGYHYGVASC EACKAFFKRT IQGNIEYSCP ATNECEITKR  
RRKSCQACRF MKCLKVGM LK EGVRLDRVRG GRQKYKRRLD SESSPYLSLQ  
ISPPAKKPLT KIVSYLLVAE PDKLYAMPPP GMPEGDIKAL TTLCDLADRE  
LVVIIGWAKH IPGFSSLSLG DQMSLLQSAW MEILILGIVY RSLPYDDKLV  
YAEDYIMDEE HSRLAGLLEL YRAILQLVRR YKKLKVEKEE FVTLKALALA  
NSDSMYIEDL EAVQKLQDLL HEALQDYELS QRHEEPWRTG KLLLTPLLR  
QTAAKAVQHF YSVKLQGVKVP MHKLFLEMLE AKAWARADSL QEWRPLEQVP  
SPLHRATKRQ HVHFLTPLPP PPSVAWVGTA QAGYHLEVFL PORAGWPRAA  
(SEQ ID NO:2)

FIGURE 3

1 GCGGGCCGCC AGTGTGGTGG AATTCGGCTT GTCACTAGGA GAACATTTGT  
51 GTTAATTGCA CTGTGCTCTG TCAAGGAAAC TTTGATTTAT AGCTGGGGTG  
101 CACAAATAAT GGTTGCCGGT CGCACATGGA TTCGGTAGAA CTTTGCCTTC  
151 CTGAATCTTT TTCCCTGCAC TACGAGGAAG AGCTTCTCTG CAGAATGTCA  
201 AACAAAGATC GACACATTGA TTCCAGCTGT TCGTCCTTCA TCAAGACGGA  
251 ACCTTCCAGC CCAGCCTCCC TGACGGACAG CGTCAACCAC CACAGCCCTG  
301 GTGGCTCTTC AGACGCCAGT GGGAGCTACA GTTCAACCAT GAATGGCCAT  
351 CAGAACGGAC TTGACTCGCC ACCTCTCTAC CTTTCTGCTC CTATCCTGGG  
401 AGGTAGTGGG CCTGTCAGGA AACTGTATGA TGACTGCTCC AGCACCATTG  
451 TTGAAGATCC CCAGACCAAG TGTGAATACA TGCTCAACTC GATGCCCCAAG  
501 AGACTGTGTT TAGTGTGTGG TGACATCGCT TCTGGGTACC ACTATGGGGT  
551 AGCATCATGT GAAGCCTGCA AGGCATTCTT CAAGAGGACA ATTCAAGGCA  
601 ATATAGAATA CAGCTGCCCT GCCACGAATG AATGTGAAAT CACAAAGCGC  
651 AGACGTAAAT CCTGCCAGGC TTGCCGCTTC ATGAAGTGTT TAAAAGTGGG  
701 CATGCTGAAA GAAGGGGTGC GTCTTGACAG AGTACGTGGA GGTCGGCAGA  
751 AGTACAAGCG CAGGATAGAT GCGGAGAACA GCCCATACCT GAACCCTCAG  
801 CTGGTTCAGC CAGCCAAAAA GCCATATAAC AAGATTGTCT CACATTTGTT  
851 GGTGGCTGAA CCGGAGAAGA TCTATGCCAT GCCTGACCCT ACTGTCCCCG  
901 ACAGTGACAT CAAAGCCCTC ACTACACTGT GTGACTTGGC CGACCGAGAG  
951 TTGGTGTTA TCATTGGATG GGCGAAGCAT ATTCCAGGCT TCTCCACGCT  
1001 GTCCCTGGCG GACCAGATGA GCCTTCTGCA GAGTGCTTGG ATGGAAATTT  
1051 TGATCCTTGG TGTCGTATAC CGGTCTCTTT CATTTGAGGA TGAACCTGTC

FIGURE 4A

1101 TATGCAGACG ATTATATAAT GGACGAAGAC CAGTCCAAAT TAGCAGGCCT  
1151 TCTTGATCTA AATAATGCTA TCCTGCAGCT GGTAAGAAA TACAAGAGCA  
1201 TGAAGCTGGA AAAAGAAGAA TTTGTCACCC TCAAAGCTAT AGCTCTTGCT  
1251 AATTCAGACT CCATGCACAT AGAAGATGTT GAAGCCGTTT AGAAGCTTCA  
1301 GGATGTCTTA CATGAAGCGC TGCAGGATTA TGAAGCTGGC CAGCACATGG  
1351 AAGACCCTCG TCGAGCTGGC AAGATGCTGA TGACACTGCC ACTCCTGAGG  
1401 CAGACCTCTA CCAAGGCCGT GCAGCATTTT TACAACATCA AACTAGAAGG  
1451 CAAAGTCCCA ATGCACAAAC TTTTTTTGGA AATGTTGGAG GCCAAGGTCT  
1501 GACTAAAAGC TCCCTGGGCC TTCCCATCCT TCATGTTGAA AAAGGGAAAA  
1551 TAAACCCAAG AGTGATGTCG AAGAACTTA GAGTTTAGTT AACAACATCA  
1601 AAAATCAACA GACTGCACTG ATAATTTAGC AGCAAGACTA TGAAGCAGCT  
1651 TTCAGATTCC TCCATAGGTT CCTGATGAGT TCTTTCTACT TTCTCCATCA  
1701 TCTTCTTTCC TCTTTCTTCC CACATTTCTC TTTCTCTTTA TTTTTTCTCC  
1751 TTTTCTTCTT TCACCTCCCT TATTTCTTTG CTTCTTTCAT TCCTAGTTCC  
1801 CATTCTCCTT TATTTTCTTC CCGTCTGCCT GCCTTCTTTC TTTTCTTTAC  
1851 CTACTCTCAT TCCTCTCTTT TCTCATCCTT CCCCTTTTTT CTAAATTGA  
1901 AATAGCTTTA GTTTAAAAA AAAAATCCTC CCTTCCCCCT TTCCTTTCCC  
1951 TTTCTTTTCT TTTTCCCTTT CCTTTTCCCT TTCCTTTCTT TTCCTCTTGA  
2001 CCTTCTTTCC ATCTTTCTTT TTCTTCCTTC TGCTGCTGAA CTTTAAAAAG  
2051 AGGTCTCTAA CTGAAGAGAG ATGGAAGCCA GCCCTGCCAA AGGATGGAGA  
2101 TCCATAATAT GGATGCCAGT GAACTTATTG TGAACCATAC CGTCCCCAAT  
2151 GACTAAGGAA TCAAAGAGAG AGAACCAACG TTCCTAAAAG TACAGTGCAA  
2201 CATATACAAA TTGACTGAGT GCAGTATTAG ATTTTCATGGG AGCAGCCTCT

FIGURE 4B

2251 AATTAGACAA CTTAAGCAAC GTTGCATCGG CTGCTTCTTA TCATTGCTTT  
2301 TCCATCTAGA TCAGTTACAG CCATTGATT CCTTAATTGT TTTTCAAGT  
2351 CTTCCAGGTA TTTGTTAGTT TAGCTACTAT GTAACTTTTT CAGGGAATAG  
2401 TTTAAGCTTT ATTCATTCAT GCAATACTAA AGAGAAATAA GAATACTGCA  
2451 ATTTTGTGCT GGCTTTGAAC AATTACGAAC AATAATGAAG GACAAATGAA  
2501 TCCTGAAGGA AGATTTTAA AAATGTTTTG TTTCTTCTTA CAAATGGAGA  
2551 TTTTTTTGTA CCAGCTTTAC CACTTTTCAG CCATTTATTA ATATGGGAAT  
2601 TTAACCTACT CAAGCAATAG TTGAAGGGAA GGTGCATATT ATCACGGATG  
2651 CAATTTATGT TGTGTGCCAG TCTGGTCCCA AACATCAATT TCTTAACATG  
2701 AGCTCCAGTT TACCTAAATG TTTACTGACA CAAAGGATGA GATTACACCT  
2751 ACAGTGACTC TGAGTAGTCA CATATATAAG CACTGCACAT GAGATATAGA  
2801 TCCGTAGAAT TGTCAGGAGT GCACCTCTCT ACTTGGGAGG TACAATTGCC  
2851 ATATGATTTT TAGCTGCCAT GGTGGTTAGG AATGTGATAC TGCCTGTTTG  
2901 CAAAGTCACA GACCTTGCCT CAGAAGGAGC TGTGAGCCAG TATTCATTTA  
2951 AGAGAATTCC ACCACACTGG CGGCCCGCGC TTGAT (SEQ ID NO:3)

FIGURE 4C

1 GCGGGCCGCCAGTGTGGTGGGAATTCGGCTTGTCACTAGGAGAACATTGTGTTAATTGCA 60  
 -----+-----+-----+-----+-----+-----+  
 CGCCCGGCGGTACACCACCTTAAGCCGAACAGTGATCCTCTTGTAACACAATTAACGT  
  
 61 CTGTGCTCTGTCAAGGAACTTTGATTTATAGCTGGGGTGCACAAATAATGGTTGCCGGT 120  
 -----+-----+-----+-----+-----+-----+  
 GACACGAGACAGTTCCTTTGAAACTAAATATCGACCCACGTGTTTATTACCAACGGCCA  
  
 121 CGCACATGGATTTCGGTAGAACTTTGCCTTCCTGAATCTTTTTCCCTGCACTACGAGGAAG 180  
 -----+-----+-----+-----+-----+-----+  
 GCGTGTACCTAAGCCATCTTGAAACGGAAGGACTTAGAAAAAGGGACGTGATGCTCCTTC  
 M D S V E L C L P E S F S L H Y E E E  
  
 181 AGCTTCTCTGCAGAATGTCAAACAAAGATCGACACATTGATTCCAGCTGTTTCGTCTTCA 240  
 -----+-----+-----+-----+-----+-----+  
 TCGAAGAGACGTCTTACAGTTTGTCTTAGCTGTGTAATAAGGTCGACAAGCAGGAAGT  
 L L C R M S N K D R H I D S S C S S F I  
  
 241 TCAAGACGGAACCTTCCAGCCCAGCCTCCCTGACGGACAGCGTCAACCACCACAGCCCTG 300  
 -----+-----+-----+-----+-----+-----+  
 AGTTCTGCCTTGGAAGGTCGGGTCGGAGGGACTGCCTGTGCGAGTTGGTGGTGTGCGGGAC  
 K T E P S S P A S L T D S V N H H S P G  
  
 301 GTGGCTCTTCAGACGCCAGTGGGAGCTACAGTTCAACCATGAATGGCCATCAGAACGGAC 360  
 -----+-----+-----+-----+-----+-----+  
 CACCGAGAAGTCTGCGGTACCCCTCGATGTCAAGTTGGTACTTACCGGTAGTCTTGCCTG  
 G S S D A S G S Y S S T M N G H Q N G L  
  
 361 TTGACTCGCCACCTCTCTACCCTTCTGCTCCTATCCTGGGAGGTAGTGGGCCTGTCAGGA 420  
 -----+-----+-----+-----+-----+-----+  
 AACTGAGCGGTGGAGAGATGGGAAGACGAGGATAGGACCCTCCATCACCCGGACAGTCCT  
 D S P P L Y P S A P I L G G S G P V R K  
  
 421 AACTGTATGATGACTGCTCCAGCACCATTTGTTGAAGATCCCCAGACCAAGTGTGAATACA 480  
 -----+-----+-----+-----+-----+-----+  
 TTGACATACTACTGACGAGGTGCTGGTAACAATTCTAGGGGTCTGGTTCACACTTATGT  
 L Y D D C S S T I V E D P Q T K C E Y M  
  
 481 TGCTCAACTCGATGCCCCAAGAGACTGTGTTTAGTGTGTGGTGACATCGCTTCTGGGTACC 540  
 -----+-----+-----+-----+-----+-----+  
 ACGAGTTGAGCTACGGGTTCTCTGACACAAATCACACACCACTGTAGCGAAGACCCATGG  
 L N S M P K R L C L V C G D I A S G Y H

FIGURE 5A

ACTATGGGGTAGCATCATGTGAAGCCTGCAAGGCATTCTTCAAGAGGACAATTCAAGGCA  
 541 -----+-----+-----+-----+-----+-----+ 600  
 TGATACCCCATCGTAGTACACTTCGGACGTTCCGTAAGAAGTTCTCCTGTAAAGTTCCGT  
Y G V A S C E A C K A F F K R T I Q G N  
 ATATAGAATACAGCTGCCCTGCCACGAATGAATGTGAAATCACAAAGCGCAGACGTAAAT  
 601 -----+-----+-----+-----+-----+-----+ 660  
 TATATCTTATGTCGACGGGACGGTGCTTACTTACACTTTAGTGTTTCGCGTCTGCATTTA  
I E Y S C P A T N E C E I T K R R R K S  
 CCTGCCAGGCTTGCCGCTTCATGAAGTGTTTAAAGTGGGCATGCTGAAAGAAGGGGTGC  
 661 -----+-----+-----+-----+-----+-----+ 720  
 GGACGGTCCGAACGGCGAAGTACTTCACAAATTTTACCCGTACGACTTTCTTCCCCACG  
C Q A C R F M K C L K V G M L K E G V R  
 GTCTTGACAGAGTACGTGGAGGTCGGCAGAAGTACAAGCGCAGGATAGATCGGGAGAACA  
 721 -----+-----+-----+-----+-----+-----+ 780  
 CAGAACTGTCTCATGCACCTCCAGCCGTCTTCATGTTTCGCGTCTATCTACGCCTCTTGT  
L D R V R G G R Q K Y K R R I D A E N S  
 GCCCATACTGAACCCTCAGCTGGTTCAGCCAGCCAAAAAGCCATATAACAAGATTGTCT  
 781 -----+-----+-----+-----+-----+-----+ 840  
 CGGGTATGGACTTGGGAGTCGACCAAGTCGGTTCGGTTTTTCGGTATATTGTTCTAACAGA  
P Y L N P Q L V Q P A K K P Y N K I V S  
 CACATTTGTTGGTGGCTGAACCGGAGAAGATCTATGCCATGCCTGACCCTACTGTCCCCG  
 841 -----+-----+-----+-----+-----+-----+ 900  
 GTGTAAACAACCACTGACTTGGCCTCTTCTAGATACGGTACGGACTGGGATGACAGGGGC  
H L L V A E P E K I Y A M P D P T V P D  
 ACAGTGACATCAAAGCCCTCACTACACTGTGTGACTTGGCCGACCGAGAGTTGGTGGTTA  
 901 -----+-----+-----+-----+-----+-----+ 960  
 TGTCAGTGTAGTTTCGGGAGTGATGTGACACACTGAACCGGCTGGCTCTCAACCACCAAT  
S D I K A L T T L C D L A D R E L V V I  
 TCATTGGATGGGCGAAGCATATTCCAGGCTTCTCCACGCTGTCCCTGGCGGACCAGATGA  
 961 -----+-----+-----+-----+-----+-----+ 1020  
 AGTAACCTACCCGCTTCGTATAAGGTCCGAAGAGGTGCGACAGGGACCGCCTGGTCTACT  
I G W A K H I P G F S T L S L A D Q M S  
 GCCTTCTGCAGAGTGCTTGGATGGAAATTTTGATCCTTGGTGTCTGATACCGGTCTCTTT  
 1021 -----+-----+-----+-----+-----+-----+ 1080  
 CGGAAGACGTCTCACGAACCTACCTTTAAACTAGGAACACAGCATATGGCCAGAGAAA  
L L Q S A W M E I L I L G V V Y R S L S

FIGURE 5B

1081 CATTGAGGATGAACTTGTCTATGCAGACGATTATATAATGGACGAAGACCAGTCCAAAT 1140  
 -----+-----+-----+-----+-----+-----+  
 GTAAACTCCTACTTGAACAGATACGTCTGCTAATATATTACCTGCTTCTGGTCAGGTTTA  
 F E D E L V Y A D D Y I M D E D Q S K L

1141 TAGCAGGCCTTCTTGATCTAAATAATGCTATCCTGCAGCTGGTAAAGAAATACAAGAGCA 1200  
 -----+-----+-----+-----+-----+-----+  
 ATCGTCCGGAAGAACTAGATTTATTACGATAGGACGTCGACCATTCTTTATGTTCTCGT  
 A G L L D L N N A I L Q L V K K Y K S M

1201 TGAAGCTGGAAAAAGAAGAATTTGTCACCCTCAAAGCTATAGCTCTTGCTAATTCAGACT 1260  
 -----+-----+-----+-----+-----+-----+  
 ACTTCGACCTTTTTCTTCTTAAACAGTGGGAGTTTCGATATCGAGAACGATTAAGTCTGA  
 K L E K E E F V T L K A I A L A N S D S

1261 CCATGCACATAGAAGATGTTGAAGCCGTTTCAAGCTTCAGGATGTCTTACATGAAGCGC 1320  
 -----+-----+-----+-----+-----+-----+  
 GGTACGTGTATCTTCTACAACCTTCGGCAAGTCTTCGAAGTCCTACAGAATGTACTTCGCG  
 M H I E D V E A V Q K L Q D V L H E A L

1321 TGCAGGATTATGAAGCTGGCCAGCACATGGAAGACCCTCGTCGAGCTGGCAAGATGCTGA 1380  
 -----+-----+-----+-----+-----+-----+  
 ACGTCCTAATACTTCGACCGGTCGTGTACCTTCTGGGAGCAGCTCGACCGTTCTACGACT  
 Q D Y E A G Q H M E D P R R A G K M L M

1381 TGACACTGCCACTCCTGAGGCAGACCTCTACCAAGGCCGTGCAGCATTTCTACAACATCA 1440  
 -----+-----+-----+-----+-----+-----+  
 ACTGTGACGGTGAGGACTCCGTCTGGAGATGGTTCCGGCACGTCGTAAAGATGTTGTAGT  
 T L P L L R Q T S T K A V Q H F Y N I K

1441 AACTAGAAGGCAAAGTCCCAATGCACAACTTTTTTTGGAAATGTTGGAGGCCAAGGTCT 1500  
 -----+-----+-----+-----+-----+-----+  
 TTGATCTTCCGTTTCAGGGTTACGTGTTTGAAAAAACCTTTACAACCTCCGGTTCCAGA  
 L E G K V P M H K L F L E M L E A K V \*  
 (SEQ ID NO:4)

1501 GACTAAAAGCTCCCTGGGCCTTCCCATCCTTCATGTTGAAAAAGGGAAAATAAACCCAAG 1560  
 -----+-----+-----+-----+-----+-----+  
 CTGATTTTCGAGGGACCCGGAAGGGTAGGAAGTACAACCTTTTTCCCTTTTATTTGGGTTC

1561 AGTGATGTCGAAGAACTTAGAGTTTAGTTAACAACATCAAAAATCAACAGACTGCACTG 1620  
 -----+-----+-----+-----+-----+-----+  
 TCACTACAGCTTCTTTGAATCTCAAATCAATTGTTGTAGTTTTTAGTTGTCTGACGTGAC

1621 ATAATTTAGCAGCAAGACTATGAAGCAGCTTTCAGATTCCTCCATAGGTTTCCTGATGAGT 1680  
 -----+-----+-----+-----+-----+-----+  
 TATTAAATCGTCGTTCTGATACTTCGTCGAAAGTCTAAGGAGGTATCCAAGGACTACTCA

FIGURE 5C



1681 TCTTTCTACTTTCTCCATCATCTTCTTTCCTCTTTCTTCCCACATTTCTCTTTCTCTTTA  
-----+-----+-----+-----+-----+ 1740  
AGAAAGATGAAAGAGGTAGTAGAAGAAAGGAGAAAGAAGGGTGTAAAGAGAAAGAGAAAT

1741 TTTTTTCTCCTTTTCTTCTTTTACCTCCCTTATTTCTTTGCTTCTTTCATTCTCTAGTTCC  
-----+-----+-----+-----+-----+ 1800  
AAAAAAGAGGAAAAGAAGAAAGTGGAGGGAATAAAGAAACGAAGAAAGTAAGGATCAAGG

1801 CATTCTCCTTTATTTTCTTCCCGTCTGCCTGCCTTCTTTCTTTTCTTTACCTACTCTCAT  
-----+-----+-----+-----+-----+ 1860  
GTAAGAGGAAATAAAAGAAGGGCAGACGGACGGAAGAAAGAAAAGAAATGGATGAGAGTA

1861 TCCTCTCTTTTCTCATCCTTCCCCTTTTTTCTAAATTTGAAATAGCTTTAGTTTAAAAAA  
-----+-----+-----+-----+-----+ 1920  
AGGAGAGAAAAGAGTAGGAAGGGGAAAAAGATTAAACTTTATCGAAATCAAATTTTTT

1921 AAAATCCTCCCTTCCCCCTTTCCTTTCCCTTTCTTTCCTTTTCCCTTTCCTTTTCCCT  
-----+-----+-----+-----+-----+ 1980  
TTTTTAGGAGGGAAGGGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGGA

1981 TTCCTTTCCCTTTCCTCTTGACCTTCTTTCATCTTCTTTTCTTCTCCTTCTGCTGCTGAA  
-----+-----+-----+-----+-----+ 2040  
AAGGAAAGGAAAGGAGAACTGGAAGAAAGGTAGAAAGAAAAGAAGGAAGACGACGACTT

2041 CTTTTAAAGAGGTCTCTAACTGAAGAGAGATGGAAGCCAGCCCTGCCAAAGGATGGAGA  
-----+-----+-----+-----+-----+ 2100  
GAAATTTTCTCCAGAGATTGACTTCTCTCTACCTTCGGTCGGGACGGTTTCCTACCTCT

2101 TCCATAATATGGATGCCAGTGAACCTTATTGTGAACCATACCGTCCCCAATGACTAAGGAA  
-----+-----+-----+-----+-----+ 2160  
AGGTATTATACCTACGGTCACTTGAATAACACTTGGTATGGCAGGGGTTACTGATTCCTT

2161 TCAAAGAGAGAGAACCAACGTTCCCTAAAAGTACAGTGCAACATATACAAATTGACTGAGT  
-----+-----+-----+-----+-----+ 2220  
AGTTTCTCTCTCTTGGTTGCAAGGATTTTCATGTCACGTTGTATATGTTTAACTGACTCA

2221 GCAGTATTAGATTTTCATGGGAGCAGCCTCTAATTAGACAACTTAAGCAACGTTGCATCGG  
-----+-----+-----+-----+-----+ 2280  
CGTCATAATCTAAAGTACCCTCGTCGGAGATTAATCTGTTGAATTCGTTGCAACGTAGCC

2281 CTGCTTCTTATCATTGCTTTTCCATCTAGATCAGTTACAGCCATTTGATTCCTTAATTGT  
-----+-----+-----+-----+-----+ 2340  
GACGAAGAATAGTAACGAAAAGGTAGATCTAGTCAATGTCGGTAAACTAAGGAATTAACA

FIGURE 5D

2341 TTTTCAAGTCTTCCAGGTATTTGTTAGTTTAGCTACTATGTAAGTCTTTTCAGGGAATAG 2400  
 -----+-----+-----+-----+-----+-----+-----+  
 AAAAAGTTTCAAGGTCCATAACAATCAAATCGATGATACATTGAAAAAGTCCCTTATC  
  
 2401 TTTAAGCTTTATTCATTCATGCAATACTAAAGAGAAATAAGAATACTGCAATTTTGTGCT 2460  
 -----+-----+-----+-----+-----+-----+-----+  
 AAATTCGAAATAAGTAAGTACGTTATGATTTCTCTTTATTCTTATGACGTTAAACACGA  
  
 2461 GGCTTTGAACAATTACGAACAATAATGAAGGACAAATGAATCCTGAAGGAAGATTTTAA 2520  
 -----+-----+-----+-----+-----+-----+-----+  
 CCGAAACTTGTTAATGCTTGTTATTACTTCCTGTTTACTTAGGACTTCCTTCTAAAAATT  
  
 2521 AAATGTTTTGTTTCTTCTTACAAATGGAGATTTTTTTGTACCAGCTTTACCACTTTTCAG 2580  
 -----+-----+-----+-----+-----+-----+-----+  
 TTTACAAAACAAGAAGAATGTTTACCTCTAAAAAACATGGTCGAAATGGTGAAAAGTC  
  
 2581 CCATTTATTAATATGGGAATTTAACTTACTCAAGCAATAGTTGAAGGGAAGGTGCATATT 2640  
 -----+-----+-----+-----+-----+-----+-----+  
 GGTAATAATTATACCCTTAAATTGAATGAGTTCGTTATCAACTTCCCTTCCACGTATAA  
  
 2641 ATCACGGATGCAATTTATGTTGTGTGCCAGTCTGGTCCCAAACATCAATTTCTTAACATG 2700  
 -----+-----+-----+-----+-----+-----+-----+  
 TAGTGCCTACGTTAAATACAACACACGGTCAGACCAGGGTTTGTAGTTAAAGAATTGTAC  
  
 2701 AGCTCCAGTTTACCTAAATGTTCACTGACACAAAGGATGAGATTACACCTACAGTGACTC 2760  
 -----+-----+-----+-----+-----+-----+-----+  
 TCGAGGTCAAATGGATTTACAAGTGAAGTGTGTTTCTACTCTAATGTGGATGTCACTGAG  
  
 2761 TGAGTAGTCACATATATAAGCACTGCACATGAGATATAGATCCGTAGAATTGTCAGGAGT 2820  
 -----+-----+-----+-----+-----+-----+-----+  
 ACTCATCAGTGTATATATTCGTGACGTGTACTCTATATCTAGGCATCTTAACAGTCCTCA  
  
 2821 GCACCTCTCTACTTGGGAGGTACAATTGCCATATGATTTCTAGCTGCCATGGTGGTTAGG 2880  
 -----+-----+-----+-----+-----+-----+-----+  
 CGTGGAGAGATGAACCTCCATGTTAACGGTATACTAAAGATCGACGGTACCACCAATCC  
  
 2881 AATGTGATACTGCCTGTTTGCAAAGTCACAGACCTTGCTCAGAAGGAGCTGTGAGCCAG 2940  
 -----+-----+-----+-----+-----+-----+-----+  
 TTACACTATGACGGACAAACGTTTTCAGTGTCTGGAACGGAGTCTTCCTCGACACTCGGTC  
  
 2941 TATTCATTTAAGAGAATTCCACCACACTGGCGGCCCGCGCTTGAT (SEQ ID NO:3) 2985  
 -----+-----+-----+-----+-----+-----+-----+  
 ATAAGTAAATTCTCTTAAGGTGGTGTGACCGCCGGGCGCGAACTA (SEQ ID NO:30)

FIGURE 5E

1 MDSVELCLPE SFSLHYEEL LCRMSNKDRH IDSSCSSFIK TEPSSPASLT  
51 DSVNHHSPGG SSDASGSYSS TMNGHQGLD SPPLYPSAPI LGGSGPVRKL  
101 YDDCSSTIVE DPQTKCEYML NSMPKRLCLV CGDIASGYHY GVASCEACKA  
151 FFKRTIQNI EYSCPATNEC EITKRRRKSC QACRFMKCLK VGMLKEGVRL  
201 DRVRGGRQKY KRRIDAENSP YLNPQLVQPA KKPYNKIVSH LLVAEPEKIY  
251 AMPDPTVPDS DIKALTTLCD LADRELVVII GWAKHIPGFS TSLADQMSL  
301 LQSAWMEILI LGVVYRSLSF EDELVEADDY IMDEDQSKLA GLLDLNNAIL  
351 QLVKKYKSMK LEKEEFVTLK AIALANSDSM HIEDVEAVQK LQDVLHEALQ  
401 DYEAGQHMED PRRAGKMLMT LPLLROTSTK AVQHFYNIKL EGKVPMHKLF  
451 LEMLEAKV\* (SEQ ID NO:4)

FIGURE 6

1 GCGGGCCGCC AGTGTGGTGG AATTCGGCTT GTCACTAGGA GAACATTTGT  
51 GTTAATTGCA CTGTGCTCTG TCAAGGAAAC TTTGATTIAT AGCTGGGGTG  
101 CACAAATAAT GGTTGCCGGT CGCACATGGA TTCGGTAGAA CTTTGCCTTC  
151 CTGAATCTTT TTCCCTGCAC TACGAGGAAG AGCTTCTCTG CAGAATGTCA  
201 AACAAAGATC GACACATTGA TTCCAGCTGT TCGTCCTTCA TCAAGACGGA  
251 ACCTTCCAGC CCAGCCTCCC TGACGGACAG CGTCAACCAC CACAGCCCTG  
301 GTGGCTCTTC AGACGCCAGT GGGAGCTACA GTTCAACCAT GAATGGCCAT  
351 CAGAACGGAC TTGACTCGCC ACCTCTCTAC CCTTCTGCTC CTATCCTGGG  
401 AGGTAGTGGG CCTGTCAGGA AACTGTATGA TGACTGCTCC AGCACCATTG  
451 TTGAAGATCC CCAGACCAAG TGTGAATACA TGCTCAACTC GATGCCCCAAG  
501 AGACTGTGTT TAGTGTGTGG TGACATCGCT TCTGGGTACC ACTATGGGGT  
551 AGCATCATGT GAAGCCTGCA AGGCATTCTT CAAGAGGACA ATTCAAGGCA  
601 ATATAGAATA CAGCTGCCCT GCCACGAATG AATGTGAAAT CACAAAGCGC  
651 AGACGTAAAT CCTGCCAGGC TTGCCGCTTC ATGAAGTGTT TAAAAGTGGG  
701 CATGCTGAAA GAAGGGGTGC GTCTTGACAG AGTACGTGGA GGTCCGGCAGA  
751 AGTACAAGCG CAGGATAGAT GCGGAGAACA GCCCATACCT GAACCCTCAG  
801 CTGGTTCAGC CAGCCAAAAA GCCATATAAC AAGATTGTCT CACATTTGTT  
851 GGTGGCTGAA CCGGAGAAGA TCTATGCCAT GCCTGACCCT ACTGTCCCCG  
901 ACAGTGACAT CAAAGCCCTC ACTACACTGT GTGACTTGGC CGACCGAGAG  
951 TTGGTGGTTA TCATTGGATG GGCGAAGCAT ATTCCAGGCT TCTCCACGCT  
1001 GTCCCTGGCG GACCAGATGA GCCTTCTGCA GAGTGCTTGG ATGGAAATTT

FIGURE 7A

1051 TGATCCTTGG TGTCGTATAC CGGTCTCTTT CATTTGAGGA TGAACCTGTC  
1101 TATGCAGACG ATTATATAAT GGACGAAGAC CAGTCCAAAT TAGCAGGCCT  
1151 TCTTGATCTA AATAATGCTA TCCTGCAGCT GGTAAGAAA TACAAGAGCA  
1201 TGAAGCTGGA AAAAGAAGAA TTTGTCACCC TCAAAGCTAT AGCTCTTGCT  
1251 AATTCAGACT CCATGCACAT AGAAGATGTT GAAGCCGTTT AGAAGCTTCA  
1301 GGATGTCTTA CATGAAGCGC TGCAGGATTA TGAAGCTGGC CAGCACATGG  
1351 AGAAGACCCT CGTCGAGCTG GCAAGATGCT GATGACACTG CCACTCCTGA  
1401 GGCAGACCTC TACCAAGGCC GTGCAGCATT TCTACAACAT CAACTAGAA  
1451 GGCAAAGTCC CAATGCACAA ACTTTTTTTTG GAAATGTTGG AGGCCAAGGT  
1501 CTGACTAAAA GCTCCCTGGG CCTTCCCATC CTTTATGTTG AAAAAGGGAA  
1551 AATAAACCCA AGAGTGATGT CGAAGAACT TAGAGTTTAG TTAACAACAT  
1601 CAAAAATCAA CAGACTGCAC TGATAATTTA GCAGCAAGAC TATGAAGCAG  
1651 CTTTCAGATT CCTCCATAGG TTCCTGATGA GTTCTTTCTA CTTTCTCCAT  
1701 CATCTTCTTT CCTCTTTCTT CCCACATTC TCTTTCTCTT TATTTTTTCT  
1751 CCTTTCTTC TTTCACCTCC CTTATTTCTT TGCTTCTTTC ATTCCTAGTT  
1801 CCCATTCTCC TTTATTTTCT TCCCGTCTGC CTGCCTTCTT TCTTTTCTTT  
1851 ACCTACTCTC ATTCCTCTCT TTTCTCATCC TTCCCCTTTT TTCTAAATTT  
1901 GAAATAGCTT TAGTTTAAAA AAAAAATCC TCCCTTCCCC CTTTCCTTTC  
1951 CCTTTCTTTC CTTTTTCCCT TTCCTTTTCC CTTTCCTTTC CTTTCCTCTT  
2001 GACCTTCTTT CCATCTTTCT TTTTCTTCCT TCTGCTGCTG AACTTTTAAA  
2051 AGAGGTCTCT AACTGAAGAG AGATGGAAGC CAGCCCTGCC AAAGGATGGA

FIGURE 7B

2101 GATCCATAAT ATGGATGCCA GTGAACTTAT TGTGAACCAT ACCGTCCCCA  
2151 ATGACTAAGG AATCAAAGAG AGAGAACCAA CGTTCCTAAA AGTACAGTGC  
2201 AACATATACA AATTGACTGA GTGCAGTATT AGATTTCATG GGAGCAGCCT  
2251 CTAATTAGAC AACTTAAGCA ACGTTGCATC GGCTGCTTCT TATCATTGCT  
2301 TTTCCATCTA GATCAGTTAC AGCCATTGA TTCCTTAATT GTTTTTTCAA  
2351 GTCTTCCAGG TATTTGTTAG TTTAGCTACT ATGTAACCTT TTCAGGGAAT  
2401 AGTTTAAGCT TTATTCATTC ATGCAATACT AAAGAGAAAT AAGAATACTG  
2451 CAATTTTGTG CTGGCTTTGA ACAATTACGA ACAATAATGA AGGACAAATG  
2501 AATCCTGAAG GAAGATTTTT AAAAATGTTT TGTTTCTTCT TACAAATGGA  
2551 GATTTTTTTG TACCAGCTTT ACCACTTTTC AGCCATTAT TAATATGGGA  
2601 ATTTAACTTA CTCAAGCAAT AGTTGAAGGG AAGGTGCATA TTATCACGGA  
2651 TGCAATTTAT GTTGTGTGCC AGTCTGGTCC CAAACATCAA TTTCTTAACA  
2701 TGAGCTCCAG TTTACCTAAA TGTTCACTGA CACAAAGGAT GAGATTACAC  
2751 CTACAGTGAC TCTGAGTAGT CACATATATA AGCACTGCAC ATGAGATATA  
2801 GATCCGTAGA ATTGTCAGGA GTGCACCTCT CTAATTGGGA GGTACAATTG  
2851 CCATATGATT TCTAGCTGCC ATGGTGGTTA GGAATGTGAT ACTGCCTGTT  
2901 TGCAAAGTCA CAGACCTTGC CTCAGAAGGA GCTGTGAGCC AGTATTCATT  
2951 TAAGAGAATT CCACCACACT GGCGGCCCGC GCTTGAT (SEQ ID NO:5)

FIGURE 7C

19999Y

1 MDSVELCLPE SFSLHYEEL LCRMSNKDRH IDSSCSSFIK TEPSSPASLT  
51 DSVNHHSPPG SSDASGSYSS TMNGHQNGLD SPPLYPSAPI LGGSGPVRKL  
101 YDDCSSTIVE DPQTKCEYML NSMPKRLCLV CGDIASGYHY GVASCEACKA  
151 FFKRTIQGNI EYSCPATNEC EITKRRRKSC QACRFMKCLK VGMLKEGVRL  
201 DRVRGGROKY KRRIDAENSP YLNPQLVQPA KKPYNKIVSH LLVAEPEKIY  
251 AMPDPTVPDS DIKALTTLCD LADRELVVII GWAKHIPGFS TSLADQMSL  
301 LQSAWMEILI LGVVYRSLSF EDELVIADDY IMDEDQSKLA GLLDLNNAIL  
351 QLVKKYKSMK LEKEEFVTLK AIALANSDSM HIEDVEAVQK LQDVLHEALQ  
401 DYEAGQHMEK TLVELARC\* (SEQ ID NO:6)

FIGURE 8

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